**Appendix**

\*estimate propensity scores and create weights;

\*denominator model;

**proc** **reg** data=cjdats.final;

model RRA\_30 = cond and list all confounders;

output out=cjdats.final student=rden;

**run**;

**quit**;

\*numerator model;

**proc** **reg** data=cjdats.final;

model RRA\_30 = cond;

output out=cjdats.final student=rnum;

**run**;

**quit**;

**data** cjdats.weights;

set cjdats.final;

pnum = exp(-**.5**\*(rnum\*\***2**))/**2.506**;

pden = exp(-**.5**\*(rden\*\***2**))/**2.506**;

wt = pnum/pden;

**run**;

\*assess balance;

**proc** **corr** data=cjdats.weights;

var RRA\_30;

with names of all confounders;

**run**;

**proc** **corr** data=cjdats.weights;

var RRA\_30;

with names of all confounders;

weight wt;

**run**;

\*outcome analysis;

**proc** **genmod** data=cjdats.weights descending;

class cid;

model condomyn= cond RRA\_30 cond\*RRA\_30 /link=logit dist=binomial;

weight wt;

repeated subject=cid/ type=indep;

**run**; **quit**;

**proc** **genmod** data=cjdats.weights;

model RRA\_30 = cond;

**run**;

**quit**;